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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 23:06:16 ; Search time 2773 Seconds

(without alignments)
5982.185 Million cell updates/sec

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Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	568.4	99.7	1219	6	AX108540 Sequence
2	568.4	99.7	1813	9	AK023655 Homo sapi
3	568.4	99.7	1960	6	AX108538 Sequence
4	568.4	99.7	2407	6	AX108534 Sequence
5	568.4	99.7	2521	6	AX108536 Sequence
6	568.4	99.7	2760	9	BC027602 Homo sapi
7	565.2	99.2	2387	9	AK093944 Homo sapi
8	377.4	66.2	2399	9	AK097718 Homo sapi
9	176	30.9	220633	9	HU091321 Human Chrom
10	176	30.9	223280	2	AC130456 Homo sapi
11	141	24.7	71596	2	AC100877 Mus muscu
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14	105.4	18.5	164564	9	HU0C003108 Human Chr
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35	42	7.4	170013	2	AC128188 Rattus no
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37	41.4	7.3	108497	2	AC094805 Rattus no
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ALIGNMENTS

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RESULT 1
AX108540      1219 bp      DNA      linear      PAT 30-APR-2001
LOCUS         Sequence 7 from Patent WO0123417.
AX108540
ACCESSION     AX108540.1 GI:13923839
VERSION
KEYWORDS
SOURCE
ORGANISM      human.
               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1219)
AUTHORS       Vinals y de Bassols,C.
TITLE         Human tumor-associated lak-4p related polynucleotides and
               polypeptides and their uses
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JOURNAL Patent: WO 0123417-A 7 05-APR-2001;
 FEATURES SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 541 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 570
 Db 544 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 573

RESULT 2
 AK023655 1813 bp mRNA linear PRI 01-AUG-2002
 LOCUS Homo sapiens cDNA FLJ13593 fis, clone PLACE1009493.
 DEFINITION AK023655
 ACCESSION AK023655
 VERSION AK023655.1 GI:10435644
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens placenta cDNA to mRNA, clone_1lb:PLACE1
 clone:PLACE1009493.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
 Nagatsuna, M., Hosoliri, T., Raku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
 Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
 Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,

TITLE Nakamura, Y., Nagahara, K., Masuno, Y., Ninomiya, K. and Iwayanagi, T.
 JOURNAL NEDO human cDNA sequencing project
 REFERENCE 2 (bases 1 to 1813)
 AUTHORS Isogai, T. and Otsuki, T.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genominfo@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction; 5'- & 3'-end one pass sequencing and clone selection;
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.

FEATURES
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 /db_xref="taxon:9606"
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BASE COUNT 489 a 400 c 405 g 519 t
 ORIGIN

Query Match 99.7%; Score 568.4; DB 9; Length 1813;
 Best Local Similarity 99.8%; Pred. No. 2.1e-147;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 481 GAGCAACAAGGCTTTTGCATTTGGGGAGACATGATGCGAGTCTTGACCTGGCATCTAGA 540
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DB 921 GAGCAACAAGGCTTTTGCATTTGGGGAGACATGATGCGAGTCTTGACCTGGCATCTAGA 990
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DB 991 AGATCAGTTCAAGAAGTAATCCAAGGGCC 1020
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LOCUS AX108538 1960 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123417.
ACCESSION AX108538
VERSION AX108538.1 GI:13923838
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1960)
AUTHORS Vinals y de Bassols, C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 5 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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source location/Qualifiers
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BASE COUNT 515 a 439 c 447 g 559 t
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Best Local Similarity 99.8%; Pred. No. 2.1e-147;
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DEFINITION Sequence 1 from Patent WO0123417.
ACCESSION AX108534
VERSION AX108534.1 GI:13923834
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2407)
AUTHORS Vinals y de Bassols, C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 1 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 2.2e-147;
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LOCUS AXI08536 2521 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 3 from Patent WO0123417.
ACCESSION AXI08536
VERSION AXI08536.1 GI:13923835
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2521)
TITLE vlnals y de Bassols,C.
JOURNAL Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
Patent: WO 0123417-A 3 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
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location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 2.2e-147;
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DB 1846 AGATCAGTTCAAGAGGTAATCCAAAGGCC 1875
RESULT 6
BC027602

LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
DEFINITION Homo sapiens, Similar to RIKEN CDNA 4932443L08 gene, clone
MGC:26648 IMAGE:4839111, mRNA, complete cds.
ACCESSION BC027602
VERSION BC027602.1 GI:20381190
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2760)
TITLE Strausberg, R.
JOURNAL Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIA-MGC Project URL: <http://mgc.nci.nih.gov>
NIA-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shrikati
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadansystemsbiology.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRK Plate: 34 Row: P Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction, Similarity but not identity to protein.
Location/Qualifiers
1..2760
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/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/tissue_type="Testis"
/clone_lib="NIA_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
213..2495
/codon_start=1
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/protein_id="AAH27602.1"
/db_xref="GI:20381191"
/translation="MISDHDVDEIIIOVENSSGVOSHPSSNOIPEKVLDSINMY
LSISDVIDDSQTSKRNDKNOVAREFSTINSESSQTLHLEMGIDTPSSSHETV
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LMSISRAYRSRNSLSEILNSISLWOKTILIGKFGSVLSYFNLRLWLFNLSF
ILNFSFIILPFTVAKNTLOFTGTEFEGVGFRTVWVYGFYNSITPDONSNGASY
NOLAVIFITGACITCFPSLFSMAKYRNNEINPHIYSGGITKLIICMDPTVHEK
AVIKOKNLSIRREMLSELROENSLTFEINOLITRSPAVMVAWVSTGAIAICAAVY
YIAEYLFELKTHSNPAGVLLPVPYSCINLAVPCISYFRIVEREYRHEVYLLI
RNIFLNTSITIGLCIYWLNTVALSGECWETLIGDITRLIMDFEFLVNSFLGFL
RRIIGQILTSGLQIEDIARVLELIVQTLVWIGIFPCPLLPFIOMIMLIMEYSK
NISLMNNEQPSKRAMSOMMEFIFLLEFPSTGVLCIATIMLKPSACGTPRG
LPLEHISYISWIDTSLRPGYLVWVYINLIGSVHFFILILVILITLYLVYQITEG
RKIMTRJHEOITINECKDKMPLIKIKIQDMKKANPSVLEREVEQGQFHLIGE
HDSGLDKRRRSVQENPRA"
BASE COUNT 739 a 637 c 625 g 759 t
ORIGIN
Query Match 99.7%; Score 568.4; DB 9; Length 2760;
Best Local Similarity 99.8%; Pred. No. 2.2e-147;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAATTTCCAGCCTCCGAGCAAGCCTGGGGGCTCAGAGATGATGACTTTTTC 60

Db 1923 ATGATGAATTTCCAGCTTCGAGCAAAAGCCTGGCGGCTCCACAGATGATGATTCTTC 1982
 QY 61 ATCTCTTGCTCTTTTCCATCTTTCCACCGGGGCTTTGTGACACCTGGCCATTCACATC 120
 Db 1983 ATCTCTTGCTCTTTTCCATCTTTCCACCGGGGCTTTGTGACACCTGGCCATTCACATC 2042
 QY 121 TGGAGATTGAAGCCTTCAGCTGCTGAGCCCTTTTCGAGTCTGCTCTTCATTCAC 180
 Db 2043 TGGAGATTGAAGCCTTCAGCTGCTGAGCCCTTTTCGAGTCTGCTCTTCATTCAC 2102
 QY 181 TCCATCTACAGCTGTGATGACACCTTAAGTACAGCGCTGCTACCTGTGGTTGTTGG 240
 Db 2103 TCCATCTACAGCTGTGATGACACCTTAAGTACAGCGCTGCTACCTGTGGTTGTTGG 2162
 QY 241 ATCTATGGAACCTTATTTGGAAGTGTGACCTTTTTCATCTCTCACTCTCATTTGCTCA 300
 Db 2163 ATCTATGGAACCTTATTTGGAAGTGTGACCTTTTTCATCTCTCACTCTCATTTGCTCA 2222
 QY 301 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 360
 Db 2223 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 2282
 QY 361 CATGAGCAGATCATTAATGAGGGGCAAAAGATAAATGTTCTGATGAAAAATTTGATCAAG 420
 Db 2283 CATGAGCAGATCATTAATGAGGGGCAAAAGATAAATGTTCTGATGAAAAATTTGATCAAG 2342
 QY 421 CTGCAAGATATGAGAAAGAAACCCAGCTCACTTGTCTGAAAAGAGAGAGTG 480
 Db 2343 CTGCAAGATATGAGAAAGAAACCCAGCTCACTTGTCTGAAAAGAGAGAGTG 2402
 QY 481 GAGCAACAAGGCTTTTTCATTTGGGGGAAACATGATGAGCTTGACCTTGAGATCTAGA 540
 Db 2403 GAGCAACAAGGCTTTTTCATTTGGGGGAAACATGATGAGCTTGACCTTGAGATCTAGA 2462
 QY 541 AGATCAGTTCAAGAAAGTAATCCAAAGGCC 570
 Db 2463 AGATCAGTTCAAGAAAGTAATCCAAAGGCC 2492

RESULT 7
 AK093944 2387 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ36625 f1s, clone TRACH2017368, weakly similar
 DEFINITION to Homo sapiens mRNA for LAK-4p.
 ACCESSION AK093944
 VERSION AK093944.1 GI:21752906
 KEYWORDS oligo capping; f1s (full insert sequence).
 SOURCE Homo sapiens trachea cDNA to mRNA, clone_l1b:TRACH2
 clone:TRACH2017368.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 1
 Sasaki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
 Shiohata, N., Matsumura, Y., Hirano, M., Sano, S., Nomura, R.,
 Yoshikawa, Y., Matsunura, Y., Moriya, S., Chiba, E., Momiyama, H.,
 Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,
 Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
 Tetsushima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
 Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Watanabe, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
 Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
 Nagahara, K., Masuko, Y., Nagai, K. and Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2387)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES
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 1. 2387
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TRACH2017368"
 /tissue_type="trachea"
 /clone_lib="TRACH2"
 /note="Cloning vector: PME18SFLU3"
 BASE COUNT 624 a 549 c 543 g 671 t
 ORIGIN

Query Match 99.2%; Score 565.2; DB 9; Length 2387;
 Best Local Similarity 99.5%; Pred. No. 176-146;
 Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATGAATTTCCAGCTTCGAGCAAAAGCCTGGCGGCTCCACAGATGATGATTCTTC 60
 Db 1025 ATGATGAATTTCCAGCTTCGAGCAAAAGCCTGGCGGCTCCACATGATGATTCTTC 1084
 QY 61 ATCTCTTGCTCTTTTCCATCTTTCCACCGGGGCTTTGTGACACCTGGCCATTCACATC 120
 Db 1085 ATCTCTTGCTCTTTTCCATCTTTCCACCGGGGCTTTGTGACACCTGGCCATTCACATC 1144
 QY 121 TGGAGATTGAAGCCTTCAGCTGCTGAGCCCTTTTCGAGTCTGCTCTTCATTCAC 180
 Db 1145 TGGAGATTGAAGCCTTCAGCTGCTGAGCCCTTTTCGAGTCTGCTCTTCATTCAC 1204
 QY 181 TCCATCTACAGCTGTGATGACACCTTAAGTACAGCGCTGCTACCTGTGGTTGTTGG 240
 Db 1205 TCCATCTACAGCTGTGATGACACCTTAAGTACAGCGCTGCTACCTGTGGTTGTTGG 1264
 QY 241 ATCTATGGAACCTTATTTGGAAGTGTGACCTTTTTCATCTCACTCTCATTTGCTCA 300
 Db 1265 ATCTATGGAACCTTATTTGGAAGTGTGACCTTTTTCATCTCACTCTCATTTGCTCA 1324
 QY 301 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 360
 Db 1325 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 1384
 QY 361 CATGAGCAGATCATTAATGAGGGGCAAAAGATAAATGTTCTGATGAAAAATTTGATCAAG 420
 Db 1385 CATGAGCAGATCATTAATGAGGGGCAAAAGATAAATGTTCTGATGAAAAATTTGATCAAG 1444
 QY 421 CTGCAAGATATGAGAAAGAAACCCAGCTCACTTGTCTGAAAAGAGAGAGTG 480
 Db 1445 CTGCAAGATATGAGAAAGAAACCCAGCTCACTTGTCTGAAAAGAGAGAGTG 1504
 QY 481 GAGCAACAAGGCTTTTTCATTTGGGGGAAACATGATGAGCTTGACCTTGAGATCTAGA 540
 Db 1505 GAGCAACAAGGCTTTTTCATTTGGGGGAAACATGATGAGCTTGACCTTGAGATCTAGA 1564
 QY 541 AGATCAGTTCAAGAAAGTAATCCAAAGGCC 570
 Db 1565 AGATCAGTTCAAGAAAGTAATCCAAAGGCC 1594

RESULT 8
 AK097718 2399 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ40399 f1s, clone TEST12037081, weakly similar
 DEFINITION to Homo sapiens mRNA for LAK-4p.
 ACCESSION AK097718
 VERSION AK097718.1 GI:21757573
 KEYWORDS oligo capping; f1s (full insert sequence).
 SOURCE Homo sapiens testis cDNA to mRNA, clone_l1b:TEST12

ORGANISM Homo sapiens
 clone:TEST12037081.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
 Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Ito, R.,
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Wagaana, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
 Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and
 Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2399)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan: cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.

FEATURES
 Source
 1. 2399
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TEST12037081"
 /issue_type="testis"
 /clone_lib="TEST12"
 /note="cloning vector: pME185FL3"

BASE COUNT 610 a 591 c 528 g 670 t

ORIGIN

Query Match 66.2%; Score 377.4; DB 9; Length 2399;
 Best Local Similarity 99.7%; Pred. No. 4e-94;
 Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGATTTCCAGCTCCGAGCAAGCCTGGCGGCTCAGAGATGATGACTTTCTC 60
 Db 1933 ATGATGATTTCCAGCTCCGAGCAAGCCTGGCGGCTCAGAGATGATGACTTTCTC 1992

QY 61 ATCTTCTGCTCTTTTCCCATCTTTACCGGGGCTTGTGCACCTGGCCATCACATC 120
 Db 1993 ATCTTCTGCTCTTTTCCCATCTTTACCGGGGCTTGTGCACCTGGCCATCACATC 2052

QY 121 TGGAGTTGAAGCCTGAGCTGAGCTGGCCCTTGGAGTCTGCTCTTCATTCAC 180
 Db 2053 TGGAGTTGAAGCCTGAGCTGAGCTGGCCCTTGGAGTCTGCTCTTCATTCAC 2112

QY 181 TCCATCTACAGCTGATGACACACCTTAAGTACAGCGGCTGCTGCTGGTTGTTGG 240
 Db 2113 TCCATCTACAGCTGATGACACACCTTAAGTACAGCGGCTGCTGCTGGTTGTTGG 2172

QY 241 ATCTATGGAACCTGATGGAAGTGTGCTCTTTTTCATCTGACCTGATTTGTGCTA 300
 Db 2173 ATCTATGGAACCTGATGGAAGTGTGCTCTTTTTCATCTGACCTGATTTGTGCTA 2232

QY 301 ATCATCAACCTATCTTACTGGCAGATCACAGAGGGAAGATTATGATTAAGCTCTC 360
 Db 2233 ATCATCAACCTATCTTACTGGCAGATCACAGAGGGAAGATTATGATTAAGCTCTC 2292

QY 361 CATGACAGATCATTAATG 379
 Db 2293 CATGACAGATCATTAATG 2311

RESULT 9
 HU091321
 LOCUS 220633 bp DNA linear PRI 10-JAN-2000
 DEFINITION Human Chromosome 16 BAC clone C1987SK-A-363E6, complete sequence.
 ACCSSION U91321
 VERSION U91321.1 GI:2951946
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R.,
 Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L.,
 Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S.,
 Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
 Genome duplications and other features in 12 Mb of DNA sequence
 from human chromosome 16p and 16q
 Genomics 60 (3), 295-308 (1999)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 10493829
 99425270
 2 (bases 1 to 220633)
 Adams, M.D., Loftus, B.J., Phillips, C.A., Zhou, L., Brandon, R.,
 Fuhrmann, J. and Venter, J.C.
 Direct Submission
 Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 3 (bases 1 to 220633)
 Adams, M.D., Loftus, B.J., Zhou, L. and Labombard, M.
 Direct Submission
 Submitted (21-MAY-1997)
 4 (bases 1 to 220633)
 Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J. and
 Venter, J.C.
 Direct Submission
 Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 5 (bases 1 to 220633)
 Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J. and
 Venter, J.C.
 Direct Submission
 Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 6 (bases 1 to 220633)
 Adams, M.D.
 Direct Submission
 Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Mar 11, 1998 this sequence version replaced gi:2335062.
 BAC clone C1987SK-363E6 is located in band 16p13.1 of chromosome
 16. Genes were identified by a combination of five methods:
 XGRAIL (available by anonymous ftp from arthur.gpm.ornl.gov),
 GeneFinder (available by anonymous ftp from
 colin@u.washington.edu), GENSCAN (available using the e-mail server
 at genSCAN@omic.stanford.edu), searches of the EST database at
 tigr (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
 peptide database. Repeats were identified using RepeatMasker (Smit,
 A.F.A. and Green, P. unpublished,
 http://ftp.genome.washington.edu/rm/RepeatMasker.html).

FEATURES
 source
 1. 220633
 Location/Qualifiers
 1. 220633
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /map="16p13.1"
 /clone="A-363E6"
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 complement(join(82033..82152,82283..82349,107848..108338))
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 complement(join(82117..82152,82283..82349,107848..107915))
 /gene="363E6.1"
 /codon_start=1

CDS
 mRNA
 gene
 CDS


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/product="Unknown gene product"
/protein_id="AAC05439.1"
/db_xref="GI:2951947"
/translation="MPTRPQPPVPRFLTSQERIHRCMCTRRLSPDAGLVLDPPASR
TIMAPSAWFLDE"
complement(217478..219568)
/gene="363B6.2"
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/db_xref="GI:2951948"
/translation="MROTDVIVITALTHRPMSLSHTDGRPRDTEFKHFFVAMDIL
LDMSMHNIWYLCISAFLMQKDFVSPAYLKKMSAKGIQVVGWTVNFDKSYESH
GSSYITDSNVEDCEPHF"

BASE COUNT      61048 a 48977 c 49108 g 61449 t      51 others
ORIGIN

Query Match      30.9%; Score 176; DB 9; Length 220633;
Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 AGATTGAAGCCTTCAGCTGCTGTCGTCCTTTTCAGAGTGCCTCTCTCATTCACATCC 183
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Db 204866 AGATTGAAGCCTTCAGCTGCTGTCGTCCTTTTCAGAGTGCCTCTCTCATTCACATCC 204925
|||||

QY 184 ATCTACAGCTGGATGACACACCTTAAGTACACAGCGCTGCTGCTGCTGCTTTGGATC 243
|||||
Db 204926 ATCTACAGCTGGATGACACACCTTAAGTACACAGCGCTGCTGCTGCTGCTTTGGATC 204985
|||||

QY 244 TATCGGAACCTCATTTGGAAGTGTGACATCTTTTCATCCCTACCCCTATTGTGCT 299
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Db 204986 TATCGGAACCTCATTTGGAAGTGTGACATCTTTTCATCCCTACCCCTATTGTGCT 205041
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RESULT 10
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LOCUS Homo sapiens chromosome 16 clone CTA-363B6, WORKING DRAFT SEQUENCE,
5 unordered pieces.
AC130456
AC130456.1 GI:22203229
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 223280)
REFERENCE DOE Joint Genome Institute.
AUTHORS DOE Joint Genome Institute.
TITLE Unpublished
JOURNAL 2 (bases 1 to 223280)
REFERENCE DOE Joint Genome Institute.
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 2773242
Center clone name: CIT978SKA_363B6
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Summary Statistics
Consensus quality: 221100 bases at least Q40
Consensus quality: 222027 bases at least Q30
Consensus quality: 222494 bases at least Q20
Estimated insert size: 220633; agarose-fp estimation
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Estimated insert size: 222880; sum-of-contigs estimation
Quality coverage: 10.81 in Q20 bases; agarose-fp estimation
Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1261: contig of 1261 bp in length
* 1262 1361: gap of unknown length
* 1362 2690: contig of 1329 bp in length
* 2691 2790: gap of unknown length
* 2791 32134: contig of 29344 bp in length
* 32135 32235: gap of unknown length
* 32235 102578: contig of 70344 bp in length
* 102579 102678: gap of unknown length
* 102679 223280: contig of 120602 bp in length.

FEATURES
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1..223280
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTA-363B6"
/clone_lib="CalTech human BAC library A"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 AGATTGAAGCCTTCAGCTGCTGTCGTCCTTTTCAGAGTGCCTCTCTCATTCACATCC 183
|||||
Db 86822 AGATTGAAGCCTTCAGCTGCTGTCGTCCTTTTCAGAGTGCCTCTCTCATTCACATCC 86881
|||||

QY 184 ATCTACAGCTGGATGACACACCTTAAGTACACAGCGCTGCTGCTGCTGCTTTGGATC 243
|||||
Db 86882 ATCTACAGCTGGATGACACACCTTAAGTACACAGCGCTGCTGCTGCTGCTTTGGATC 86941
|||||

QY 244 TATCGGAACCTCATTTGGAAGTGTGACATCTTTTCATCCCTACCCCTATTGTGCT 299
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Db 86942 TATCGGAACCTCATTTGGAAGTGTGACATCTTTTCATCCCTACCCCTATTGTGCT 86997
|||||

RESULT 11
AC100877 71596 bp DNA linear HTG 23-NOV-2001
LOCUS Mus musculus clone RP23-35B17, LOW-PASS SEQUENCE SAMPLING.
AC100877
AC100877.1 GI:17059651
VERSION HTG; HTGS_PHASE0.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 71596)
REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
AUTHORS Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouknight, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gaidyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Huime, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
```

TITLE
JOURNAL
COMMENT

Maclean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Plerer,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thoman,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center Project name: L13918

Center clone name: 35_B_17

* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 723 822: contig of 722 bp in length
* 823 1526: gap of 100 bp
* 1527 1626: contig of 704 bp in length
* 1627 2336: contig of 710 bp in length
* 2337 2436: gap of 100 bp
* 2437 3156: contig of 720 bp in length
* 3157 3256: gap of 100 bp
* 3257 3984: contig of 728 bp in length
* 3985 4084: gap of 100 bp
* 4085 4811: contig of 727 bp in length
* 4812 4911: gap of 100 bp
* 4912 5638: contig of 727 bp in length
* 5639 5738: gap of 100 bp
* 5739 6477: contig of 739 bp in length
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* 6578 7305: contig of 728 bp in length
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* 7406 8107: contig of 702 bp in length
* 8108 8207: gap of 100 bp
* 8208 8950: contig of 743 bp in length
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* 9051 9743: contig of 693 bp in length
* 9744 9843: gap of 100 bp
* 9844 10583: contig of 740 bp in length
* 10584 10683: gap of 100 bp
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* 13070 13169: gap of 100 bp
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* 13952 14685: contig of 734 bp in length

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* 38522 38621: gap of 100 bp
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Best Local Similarity 97.08; Pred. No. 1.9e-24;
Matches 129; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGATGAAATTTCCAGCCCTCCGAGCAAAAGCCGCGGCGGCGCTCACAGATGATGACTTTCTTC 60
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|||||

QY 61 ATCTCTTGTGCTTTTTCACATCTTTCACGCGGGGCTTTGTSCACCCCTGGCCATCCACATC 120
|||||
Db 329 ATCTCTTGTGCTTTTTCACATCTTTCACGCGGGGCTTTGTSCACCCCTGGCCATCCACATC 388
|||||

QY 121 TGGAGATTGAAGC 133
|||||
Db 389 TTGAGATTGAAGC 401

RESULT 13
AC124444_2/c
WPCOMMENT
Sequence split into 5 fragments
Fragment Name      Begin      End      LOCUS AC124444 Accession AC124444
1
AC124444_0      10000      210000
AC124444_1      100001      310000
AC124444_2      200001      410000
AC124444_3      300001      410000
AC124444_4      400001      410492

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RESULT	13
AC124444_2/c	
MPCOMMENT	
Sequence split into 5 fragments	
Fragment Name	Begin End
AC124444_0	1 110000
AC124444_1	100001 210000
AC124444_2	200001 310000
AC124444_3	300001 410000
AC124444_4	400001 410492
Continuation (3 of 5) of AC124444	from base 200001 (AC124444 Mus musculus chromosome)

RESULT	14				
LOCUS	HUAC003108				
DEFINITION	Human Chromosome 16 BAC clone C1987SK-327024, complete sequence.	164564 bp	DNA	linear	PRI 23-NOV-1999
ACCESSION	AC003108				
VERSION	AC003108.1	GI:2833632			
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 164564)				
AUTHORS	Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Deslattes,Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.				
TITLE	Genome duplications and other features in 12 MD of DNA sequence from human chromosome 16p and 16q				
JOURNAL	Genomics 60 (3), 295-308 (1999)				
MEDLINE	99425270				

FEATURE	SOURCE
PUBMED	10493829
REFERENCE	2 (bases 1 to 164564)
AUTHORS	Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
TITLE	Human Chromosome 16 BAC clone C19875K-327024
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 164564)
AUTHORS	Adams,M.D. and Loftus,B.J.
TITLE	Direct Submission
JOURNAL	Submitted (19-NOV-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, Email: bjoftus@tigr.org
REFERENCE	4 (bases 1 to 164564)
AUTHORS	Adams,M.D.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
REFERENCE	5 (bases 1 to 164564)
AUTHORS	Adams,M.D. and Loftus,B.J.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
COMMENT	On Feb 5, 1998 this sequence version replaced gi:2827780. Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: mda@tigr.org. The orientation of the sequence is from Spe end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of Washington), GenScan (Chris Burge, http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the complete sequence against a peptide database, and the Human gene index database at TIGR (http://www.tigr.org/tcd/hg1/hg1.html). Genes without peptide homology having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/) location/Qualifiers
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BASE COUNT 45464 a 34232 c 36100 g 48768 t

ORIGIN

Query Match 18.5% Score 105.4; DB 9; Length 164564;
 Best Local Similarity 99.1%; Pred. No. 4,7e-18;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 377 ATGAGGGCGAAGATPAAATGTTCCGATGAGAAAAATTGATCAAGCTGCAGATATGAGGA 436
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 Db 1258 AGAAAGCAAAACCCAGCTACTTGTTCGTGAAGAAGAGAGAGGTGAG 1304
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RESULT 15
 LOCUS AB002405 1639 bp mRNA linear PRI 02-MAR-2000
 DEFINITION Homo sapiens mRNA for LAK-4p, complete cds.
 ACCESSION AB002405
 VERSION AB002405.2 GI:7209573
 KEYWORDS LAK-4p.
 SOURCE Homo sapiens male lymphoid mLT expressing LAK cell cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1639)
 AUTHORS Abe,Y. and Takaoka,Y.
 TITLE LAK-4 clone from the membrane lymphotoxin expressing subtraction
 library
 JOURNAL Published Only in Database (1998)
 REFERENCE 2 (bases 1 to 1639)
 AUTHORS Abe,Y. and Takaoka,Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Yasuhiro Abe, Ehime University School of
 Medicine, The Second Department of Surgery, Shigenobu, Onsen-gun,
 Ehime 791-02, Japan (E-mail:yasuhiro@ehime-u.ac.jp,
 Tel:++81-89-964-5111, Fax:++81-89-960-5334)
 COMMENT On Mar 8, 2000 this sequence version replaced gi:2760120.
 Sequence updated (05-Jan-1998)
 Sequence updated (29-Feb-2000).
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 location/Qualifiers
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52.68; Pred. No. 6.6e-17;

conservative 0; Mismatches 216; Indels 3; Gaps 1;

ACAGCCCTCCGAGCAAGCCCTGGCCGGCCCTCAGATGATGACCTTTCTTCA 61

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BASE COUNT	294 a	495 c
ORIGIN	517 g	333 t

BASE COUNT	294 a	495 c	517 g	333 t
ORIGIN				

ORIGIN

Query Match	17.6%;	Score 100.4;	DB 9;	Length 1639;
Best Local Similarity	52.6%;	Pred. No. 6.6e-17;		
Matches 243; Conservative	0;	Mismatches 216;	Indels 3;	Gaps 1;

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Db 867 TGGCAACTGCCAGGCGCGGCCCTGGCTGGCTCACACATGAGCACCGTCTCC 922

62 TCTTCTTGCTTTTCCCATCTTCACCGGGTCTTGTCACCCCTGGCCATCACCATCT 12

Db 927 TCACGCTGCTCTGCTTCCCCGCGCTTCCCTGGGCGCGCTGTCCTTCCCTCTGCTACGCGGCT 98

122 GGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCCTGCCCTCTTCATTCACT 18

Db 987 GGCAGGTGAAAGCCCTGAGCAGCTGCGGCGCCCTTCGAGACCTGAGACCTGATGTAAGAG 1000

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